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Sequence Listing could not be accepted due to errors.

See attached Validation Report.

If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=12; day=5; hr=15; min=11; sec=1; ms=756;]

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Reviewer Comments:

<210> 1

<211> 4620

<212> DNA

<213> Homo sapien

Please change the above <213> response to "Homo sapiens". This misspelling also appears in subsequent sequences.

<210> 5

<211> 21

<212> oligonucleotide

<213> artificial sequence

<220>

<223> primers for c-met

<400> 5

agccagtaat gatctcaata g

21

The above <212> response is invalid: use DNA instead. Same error in Sequences 6-8.

Application No: 10599327 Version No: 1.0

Input Set:

Output Set:

Started: 2008-11-17 18:50:41.779
Finished: 2008-11-17 18:50:43.119
Elapsed: 0 hr(s) 0 min(s) 1 sec(s) 340 ms
Total Warnings: 9
Total Errors: 4
No. of SeqIDs Defined: 18
Actual SeqID Count: 18

| Error code | Error Description |
|------------|--|
| W 402 | Undefined organism found in <213> in SEQ ID (1) |
| W 402 | Undefined organism found in <213> in SEQ ID (2) |
| E 310 | Invalid sequence type in <212> in SEQID: (5) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (5) |
| E 310 | Invalid sequence type in <212> in SEQID: (6) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (6) |
| E 310 | Invalid sequence type in <212> in SEQID: (7) |
| W 213 | Artificial or Unknown found in <213> in SEQ ID (7) |
| E 310 | Invalid sequence type in <212> in SEQID: (8) |
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| W 402 | Undefined organism found in <213> in SEQ ID (13) |
| W 402 | Undefined organism found in <213> in SEQ ID (14) |
| W 402 | Undefined organism found in <213> in SEQ ID (15) |

SEQUENCE LISTING

<110> Van Andel Research Institute
Shinomiya et al., Nariyoshi

<120> c-met siRNA ADENOVIRUS VECTORS INHIBIT CANCER CELL GROWTH,
INVASION AND TUMORIGENICITY

<130> VAN067 P-328A

<140> 10599327

<141> 2008-11-17

<150> 60/556,473

<151> 2004-03-26

<160> 18

<170> PatentIn version 3.5

<210> 1

<211> 4620

<212> DNA

<213> Homo sapien

<400> 1

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| gcgcgtgtgg tccttgcgcc gctgacttct ccaactggttc ctgggcaccg aaagataaac | 180 |
| ctctcataat gaaggccccc gctgtgcttg cacctggcat cctcgtgctc ctgtttacct | 240 |
| tggtgcagag gagcaatggg gagtgtaaag aggactagc aaagtccgag atgaatgtga | 300 |
| atatgaagta tcagcttccc aacttcaccg cggaacacc catccagaat gtcattctac | 360 |
| atgagcatca cattttcctt ggtgccacta actacattta tgttttaaat gaggaagacc | 420 |
| ttcagaaggt tgctgagtac aagactgggc ctgtgctgga acaccagat tgtttcccat | 480 |
| gtcaggactg cagcagcaaa gccaatatat caggaggtgt ttggaaagat aacatcaaca | 540 |
| tggtcttagt tgtcgacacc tactatgatg atcaactcat tagctgtggc agcgtcaaca | 600 |
| gagggacctg ccagcgacat gtctttcccc acaatcatat tgctgacata cagtcggagg | 660 |
| ttcactgcat atttccccca cagatagaag agcccagcca gtgtcctgac tgtgtggtga | 720 |
| gcgccttggg agccaaagtc ctttcatctg taaaggaccg gttcatcaac ttctttgtag | 780 |
| gcaataccat aaattcttct tatttcccag atcatccatt gcattcgata tcagtgagaa | 840 |
| ggctaaagga aacgaaagat ggttttatgt ttttgacgga ccagtcctac attgatgttt | 900 |

| | |
|--|------|
| tacctgagtt cagagattct taccocatta agtatgtcca tgcctttgaa agcaacaatt | 960 |
| ttatttactt cttgacggtc caaagggaaa ctctagatgc tcagactttt cacacaagaa | 1020 |
| taatcaggtt ctgttccata aactctggat tgcattccta catggaaatg cctctggagt | 1080 |
| gtattctcac agaaaagaga aaaaagagat ccacaaagaa ggaagtgttt aatatacttc | 1140 |
| aggctgcgta tgtcagcaag cctggggccc agcttgctag acaaataagga gccagcctga | 1200 |
| atgatgacat tcttttcggg gtgttcgcac aaagcaagcc agattctgcc gaaccaatgg | 1260 |
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| cagagggctcg cttcatgcag gttgtggttt ctcgatcagg accatcaacc cctcatgtga | 1620 |
| attttctcct ggactcccat ccagtgtctc cagaagtgat tgtggagcat acattaaacc | 1680 |
| aaaatggcta cacactgggt atcactggga agaagatcac gaagatccca ttgaatggct | 1740 |
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| aacagatctg tctgctgca atctacaagg ttttccaaa tagtgacccc cttgaaggag | 1920 |
| ggacaagggt gaccatatgt ggctgggact ttggatttcg gaggaataat aaatttgatt | 1980 |
| taaagaaaac tagagttctc cttggaaatg agagctgcac cttgacttta agtgagagca | 2040 |
| cgatgaatac attgaaatgc acagttggtc ctgccatgaa taagcatttc aatatgtcca | 2100 |
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| taataacaag tatttcgccg aaatacggtc ctatggctgg tggcacttta cttactttaa | 2220 |
| ctggaaatta cctaaacagt ggaattcta gacacatttc aattggtgga aaaacatgta | 2280 |
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| accgtgaaga tcccattgtc tatgaaattc atccaaccaa atcttttatt agtacttggg | 2460 |
| ggaaagaacc tctcaacatt gtcagttttc tattttgctt tgccagtggg gggagcacia | 2520 |
| taacaggtgt tgggaaaaac ctgaattcag ttagtgtccc gagaatggtc ataaatgtgc | 2580 |
| atgaagcagg aaggaacttt acagtggcat gtcaacatcg ctctaattca gagataatct | 2640 |

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| gttgtagcac | tccttcctg | caacagctga | atctgcaact | ccccctgaaa | accaaagcct | 2700 |
| ttttcatgtt | agatgggatc | ctttccaaat | actttgatct | catttatgta | cataatcctg | 2760 |
| tgtttaagcc | ttttgaaaag | ccagtgatga | tctcaatggg | caatgaaaat | gtactggaaa | 2820 |
| ttaagggaaa | tgatattgac | cctgaagcag | ttaaagggtga | agtgttaaaa | gttggaata | 2880 |
| agagctgtga | gaatatacac | ttacattctg | aagccgtttt | atgcacgggc | cccaatgacc | 2940 |
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| ttggaaaagt | aatagttcaa | ccagatcaga | atttcacagg | attgattgct | gggtgtgtct | 3060 |
| caatatcaac | agcactgtta | ttactacttg | ggtttttcct | gtggctgaaa | aagagaaaagc | 3120 |
| aaattaaaga | tctgggcagt | gaattagttc | gctacgatgc | aagagtacac | actcctcatt | 3180 |
| tggataggct | tgtaagtgcc | cgaagtgtaa | gcccactac | agaaatgggt | tcaaatgaat | 3240 |
| ctgtagacta | ccgagctact | tttcagaag | atcagtttcc | taattcatct | cagaacggtt | 3300 |
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| aaacaggtgc | aaagctgcca | gtgaagtgga | tggctttgga | aagtctgcaa | actcaaaagt | 4020 |
| ttaccaccaa | gtcagatgtg | tggctccttg | gcgtcgctct | ctgggagctg | atgacaagag | 4080 |
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| gaagactcct | acaacccgaa | tactgccag | acccttata | tgaagtaatg | ctaaaatgct | 4200 |
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| tcttctctac | tttcattggg | gagcactatg | tccatgtgaa | cgctacttat | gtgaacgtaa | 4320 |

| | | | | | | |
|------------|------------|------------|------------|------------|------------|------|
| aatgtgtcgc | tccgtatcct | tctctgttgt | catcagaaga | taacgctgat | gatgaggtgg | 4380 |
| acacacgacc | agcctccttc | tgggagacat | catagtgcta | gtactatgtc | aaagcaacag | 4440 |
| tccacacttt | gtccaatggg | tttttactg | cctgaccttt | aaaaggccat | cgatattctt | 4500 |
| tgctccttgc | cataggactt | gtattgttat | ttaaattact | ggattctaag | gaatttctta | 4560 |
| tctgacagag | catcagaacc | agaggcttgg | tcccacaggc | cagggaccaa | tgcgctgcag | 4620 |

Met Lys Ala Pro Ala Val Leu Ala Pro Gly Ile Leu Val Leu Leu Phe
1 5 10 15

Glu Thr Pro Ile Gln Asn Val Ile Leu His Glu His His Ile Phe Leu
50 55 60

Pro Cys Gln Asp Cys Ser Ser Lys Ala Asn Leu Ser Gly Gly Val Trp
100 105 110

| | | | | | | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Val | Phe | Pro | His | Asn | His | Thr | Ala | Asp | Ile | Gln | Ser | Glu | Val | His | Cys |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |

| | | |
|---|-----|---------|
| Ile Phe Ser Pro Gln Ile Glu Glu Pro Ser Gln Cys Pro Asp Cys Val | | |
| 165 | 170 | 175 |
| Val Ser Ala Leu Gly Ala Lys Val Leu Ser Ser Val Lys Asp Arg Phe | | |
| 180 | 185 | 190 |
| Ile Asn Phe Phe Val Gly Asn Thr Ile Asn Ser Ser Tyr Phe Pro Asp | | |
| 195 | 200 | 205 |
| His Pro Leu His Ser Ile Ser Val Arg Arg Leu Lys Glu Thr Lys Asp | | |
| 210 | 215 | 220 |
| Gly Phe Met Phe Leu Thr Asp Gln Ser Tyr Ile Asp Val Leu Pro Glu | | |
| 225 | 230 | 235 240 |
| Phe Arg Asp Ser Tyr Pro Ile Lys Tyr Val His Ala Phe Glu Ser Asn | | |
| 245 | 250 | 255 |
| Asn Phe Ile Tyr Phe Leu Thr Val Gln Arg Glu Thr Leu Asp Ala Gln | | |
| 260 | 265 | 270 |
| Thr Phe His Thr Arg Ile Ile Arg Phe Cys Ser Ile Asn Ser Gly Leu | | |
| 275 | 280 | 285 |
| His Ser Tyr Met Glu Met Pro Leu Glu Cys Ile Leu Thr Glu Lys Arg | | |
| 290 | 295 | 300 |
| Lys Lys Arg Ser Thr Lys Lys Glu Val Phe Asn Ile Leu Gln Ala Ala | | |
| 305 | 310 | 315 320 |
| Tyr Val Ser Lys Pro Gly Ala Gln Leu Ala Arg Gln Ile Gly Ala Ser | | |
| 325 | 330 | 335 |
| Leu Asn Asp Asp Ile Leu Phe Gly Val Phe Ala Gln Ser Lys Pro Asp | | |
| 340 | 345 | 350 |
| Ser Ala Glu Pro Met Asp Arg Ser Ala Met Cys Ala Phe Pro Ile Lys | | |
| 355 | 360 | 365 |
| Tyr Val Asn Asp Phe Phe Asn Lys Ile Val Asn Lys Asn Asn Val Arg | | |
| 370 | 375 | 380 |

Cys Leu Gln His Phe Tyr Gly Pro Asn His Glu His Cys Phe Asn Arg
385 390 395 400

Thr Leu Leu Arg Asn Ser Ser Gly Cys Glu Ala Arg Arg Asp Glu Tyr
405 410 415

Arg Thr Glu Phe Thr Thr Ala Leu Gln Arg Val Asp Leu Phe Met Gly
420 425 430

Gln Phe Ser Glu Val Leu Leu Thr Ser Ile Ser Thr Phe Ile Lys Gly
435 440 445

Asp Leu Thr Ile Ala Asn Leu Gly Thr Ser Glu Gly Arg Phe Met Gln
450 455 460

Val Val Val Ser Arg Ser Gly Pro Ser Thr Pro His Val Asn Phe Leu
465 470 475 480

Leu Asp Ser His Pro Val Ser Pro Glu Val Ile Val Glu His Thr Leu
485 490 495

Asn Gln Asn Gly Tyr Thr Leu Val Ile Thr Gly Lys Lys Ile Thr Lys
500 505 510

Ile Pro Leu Asn Gly Leu Gly Cys Arg His Phe Gln Ser Cys Ser Gln
515 520 525

Cys Leu Ser Ala Pro Pro Phe Val Gln Cys Gly Trp Cys His Asp Lys
530 535 540

Cys Val Arg Ser Glu Glu Cys Leu Ser Gly Thr Trp Thr Gln Gln Ile
545 550 555 560

Cys Leu Pro Ala Ile Tyr Lys Val Phe Pro Asn Ser Ala Pro Leu Glu
565 570 575

Gly Gly Thr Arg Leu Thr Ile Cys Gly Trp Asp Phe Gly Phe Arg Arg
580 585 590

Asn Asn Lys Phe Asp Leu Lys Lys Thr Arg Val Leu Leu Gly Asn Glu
595 600 605

Ser Cys Thr Leu Thr Leu Ser Glu Ser Thr Met Asn Thr Leu Lys Cys

| | | |
|---|-----|---------|
| 610 | 615 | 620 |
| Thr Val Gly Pro Ala Met Asn Lys His Phe Asn Met Ser Ile Ile Ile | | |
| 625 | 630 | 635 640 |
| Ser Asn Gly His Gly Thr Thr Gln Tyr Ser Thr Phe Ser Tyr Val Asp | | |
| | 645 | 650 655 |
| Pro Val Ile Thr Ser Ile Ser Pro Lys Tyr Gly Pro Met Ala Gly Gly | | |
| | 660 | 665 670 |
| Thr Leu Leu Thr Leu Thr Gly Asn Tyr Leu Asn Ser Gly Asn Ser Arg | | |
| | 675 | 680 685 |
| His Ile Ser Ile Gly Gly Lys Thr Cys Thr Leu Lys Ser Val Ser Asn | | |
| | 690 | 695 700 |
| Ser Ile Leu Glu Cys Tyr Thr Pro Ala Gln Thr Ile Ser Thr Glu Phe | | |
| 705 | 710 | 715 720 |
| Ala Val Lys Leu Lys Ile Asp Leu Ala Asn Arg Glu Thr Ser Ile Phe | | |
| | 725 | 730 735 |
| Ser Tyr Arg Glu Asp Pro Ile Val Tyr Glu Ile His Pro Thr Lys Ser | | |
| | 740 | 745 750 |
| Phe Ile Ser Thr Trp Trp Lys Glu Pro Leu Asn Ile Val Ser Phe Leu | | |
| | 755 | 760 765 |
| Phe Cys Phe Ala Ser Gly Gly Ser Thr Ile Thr Gly Val Gly Lys Asn | | |
| | 770 | 775 780 |
| Leu Asn Ser Val Ser Val Pro Arg Met Val Ile Asn Val His Glu Ala | | |
| 785 | 790 | 795 800 |
| Gly Arg Asn Phe Thr Val Ala Cys Gln His Arg Ser Asn Ser Glu Ile | | |
| | 805 | 810 815 |
| Ile Cys Cys Thr Thr Pro Ser Leu Gln Gln Leu Asn Leu Gln Leu Pro | | |
| | 820 | 825 830 |
| Leu Lys Thr Lys Ala Phe Phe Met Leu Asp Gly Ile Leu Ser Lys Tyr | | |
| | 835 | 840 845 |

Phe Asp Leu Ile Tyr Val His Asn Pro Val Phe Lys Pro Phe Glu Lys
850 855 860

Pro Val Met Ile Ser Met Gly Asn Glu Asn Val Leu Glu Ile Lys Gly
865 870 875 880

Asn Asp Ile Asp Pro Glu Ala Val Lys Gly Glu Val Leu Lys Val Gly
885 890 895

Asn Lys Ser Cys Glu Asn Ile His Leu His Ser Glu Ala Val Leu Cys
900 905 910

Thr Val Pro Asn Asp Leu Leu Lys Leu Asn Ser Glu Leu Asn Ile Glu
915 920 925

Trp Lys Gln Ala Ile Ser Ser Thr Val Leu Gly Lys Val Ile Val Gln
930 935 940

Pro Asp Gln Asn Phe Thr Gly Leu Ile Ala Gly Val Val Ser Ile Ser
945 950 955 960

Thr Ala Leu Leu Leu Leu Leu Gly Phe Phe Leu Trp Leu Lys Lys Arg
965 970 975

Lys Gln Ile Lys Asp Leu Gly Ser Glu Leu Val Arg Tyr Asp Ala Arg
980 985 990

Val His Thr Pro His Leu Asp Arg Leu Val Ser Ala Arg Ser Val Ser
995 1000 1005

Pro Thr Thr Glu Met Val Ser Asn Glu Ser Val Asp Tyr Arg Ala
1010 1015 1020

Thr Phe Pro Glu Asp Gln Phe Pro Asn Ser Ser Gln Asn Gly Ser
1025 1030 1035

Cys Arg Gln Val Gln Tyr Pro Leu Thr Asp Met Ser Pro Ile Leu
1040 1045 1050

Thr Ser Gly Asp Ser Asp Ile Ser Ser Pro Leu Leu Gln Asn Thr
1055 1060 1065

| | | | |
|---------|---------------------|---------------------|-------------|
| Val His | Ile Asp Leu Ser Ala | Leu Asn Pro Glu Leu | Val Gln Ala |
| 1070 | 1075 | 1080 | |
| Val Gln | His Val Val Ile Gly | Pro Ser Ser Leu Ile | Val His Phe |
| 1085 | 1090 | 1095 | |
| Asn Glu | Val Ile Gly Arg Gly | His Phe Gly Cys Val | Tyr His Gly |
| 1100 | 1105 | 1110 | |
| Thr Leu | Leu Asp Asn Asp Gly | Lys Lys Ile His Cys | Ala Val Lys |
| 1115 | 1120 | 1125 | |
| Ser Leu | Asn Arg Ile Thr Asp | Ile Gly Glu Val Ser | Gln Phe Leu |
| 1130 | 1135 | 1140 | |
| Thr Glu | Gly Ile Ile Met Lys | Asp Phe Ser His Pro | Asn Val Leu |
| 1145 | 1150 | 1155 | |
| Ser Leu | Leu Gly Ile Cys Leu | Arg Ser Glu Gly Ser | Pro Leu Val |
| 1160 | 1165 | 1170 | |
| Val Leu | Pro Tyr Met Lys His | Gly Asp Leu Arg Asn | Phe Ile Arg |
| 1175 | 1180 | 1185 | |
| Asn Glu | Thr His Asn Pro Thr | Val Lys Asp Leu Ile | Gly Phe Gly |
| 1190 | 1195 | 1200 | |
| Leu Gln | Val Ala Lys Ala Met | Lys Tyr Leu Ala Ser | Lys Lys Phe |
| 1205 | 1210 | 1215 | |
| Val His | Arg Asp Leu Ala Ala | Arg Asn Cys Met Leu | Asp Glu Lys |
| 1220 | 1225 | 1230 | |
| Phe Thr | Val Lys Val Ala Asp | Phe Gly Leu Ala Arg | Asp Met Tyr |
| 1235 | 1240 | 1245 | |
| Asp Lys | Glu Tyr Tyr Ser Val | His Asn Lys Thr Gly | Ala Lys Leu |
| 1250 | 1255 | 1260 | |
| Pro Val | Lys Trp Met Ala Leu | Glu Ser Leu Gln Thr | Gln Lys Phe |
| 1265 | 1270 | 1275 | |

Thr Thr Lys Ser Asp Val Trp Ser Phe Gly Val Val Leu Trp Glu
1280 1285 1290

Leu Met Thr Arg Gly Ala Pro Pro Tyr Pro Asp Val Asn Thr Phe
1295 1300 1305

Asp Ile Thr